

PCT09

RAW SEQUENCE LISTING

DATE: 10/17/2001

PATENT APPLICATION: US/09/787,016A

TIME: 13:11:26

Input Set : N:\Crf3\09272001\I787016.raw

Output Set: N:\CRF3\10172001\I787016A.raw

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1 <110> APPLICANT: Alonso, Carlos
 2 Domingo, David
 3 Grandien, Alf
 4 Leonardo, Esther
 5 Martinez, Pedro
 6 <120> TITLE OF INVENTION: Genes Encoding for the Human and Murine Death Inducer-
 Obliterator-1
 7 <130> FILE REFERENCE: 46309-253995
 8 <140> CURRENT APPLICATION NUMBER: US/09/787,016A
 9 <141> CURRENT FILING DATE: 2001-06-18
 10 <150> PRIOR APPLICATION NUMBER: PCT/GB99/03019
 11 <151> PRIOR FILING DATE: 1999-09-10
 12 <160> NUMBER OF SEQ ID NOS: 4
 13 <170> SOFTWARE: PatentIn version 3.0
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 2610
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Homo sapiens
 19 <400> SEQUENCE: 1

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22	cctgttactc	gtgaacagtg	gctgacaaca	gtgttggtgt	gagcctggct	gtctgcttgg	180
23	accagagagt	ttcgtctgcc	agggtttttg	gttgatttta	ggatttcagg	gaaaagtgtc	240
24	caagctttca	gtgttgagc	aggtatggac	gacaaaggcg	acccgagcaa	tgaggaggca	300
25	cctaaggcca	tcaaaccac	cagcaaagag	ttcaggaaaa	catggggttt	tcgaaggacc	360
26	actatcgcca	agcgagagg	cgcaggggac	gcggaggctg	acccactgga	gccgccaccc	420
27	ccacagcagc	agctgggcct	gtccctgcgg	cgcagtggga	ggcagcccaa	gcgcactgag	480
28	cgcgtggagc	agttcctgac	cattgcgcgg	cgccgcggca	ggaggagcat	gcctgtctcc	540
29	ctggagggatt	ctggtgagcc	cacgtcctgc	cccgccacag	acgccgagac	agcctccgag	600
30	ggcagcgtgg	aaagcgcttc	tgagaccaga	agcggccccc	agtctgcttc	cacagctgtg	660
31	aaggaaacgac	cagcctcttc	tgaaaagggtg	aaaggagggg	atgaccacga	tgacacctcc	720
32	gatagtgaca	gcgatggcct	gaccttgaaa	gagcttcaga	atcgccctcg	caggaagcgg	780
33	gaacaggagc	ccactgagag	gcccctgaaa	gggatccaga	gtcgcctgcg	gaagaagcgc	840
34	cgggaggagg	gtcccgccga	gactgtgggc	tccgaggcca	gtgacactgt	ggagggcgtc	900
35	ctgcccagta	agcaggagcc	cgagaacgat	caggggggtt	tgtcccaggc	tgggaaagat	960
36	gacagagaga	gtaagtggga	gggaaaggcg	gctcaggaca	tcaaagatga	ggagcctgga	1020
37	gacttggggc	gaccgaagcc	tgaatgtgag	ggttacgacc	ccaacgccct	gtattgcatt	1080
38	tgccgcgagc	ctcacaacaa	caggtttatg	atttgctgtg	accgctgtga	agaatgggtt	1140
39	catggcgatt	gtgtgggcat	ttctgaggct	cgagggaggc	ttttggaaa	gaatggggaa	1200
40	gactatatct	gccccaaactg	caccattctg	caagtgcagg	atgagactca	ttcagaaaacg	1260
41	gcagatcagc	aggaagctaa	atggagacct	ggagatgctg	atggcaccga	ttgtacaagt	1320
42	ataggaacaa	tagagcagaa	gtctagcgaa	gaccaaggga	taaagggtag	aattgagaaa	1380
43	gctgcaaadc	caagtggcaa	gaagaaactc	aagatcttcc	agcctgtgat	agaggcgcct	1440
44	ggtgcctcaa	aatgtattgg	ccccgggtgc	tgtcacgtgg	cgcagcccga	ctcgggtgtac	1500
45	tgcagtaatg	actgtatcct	caaacacgcc	gcagcgacaa	tgaagtttct	aagctcaggt	1560
46	aaagaacaga	agccaaagcc	taaagaaaag	atgaagatga	agccagagaa	gcccagtcct	1620
47	ccgaaatgcg	gtgctcaggc	aggattataa	atctcttctg	tgacacaagag	accagctcca	1680
48	gaaaaaaaaa	agaccacagt	gaagaaggca	gtggtggtcc	ctgcgcggag	tgaagcactc	1740

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51	cacctagggg	ttggcctcct	ggacccctcc	cgttctttct	ggatagccat	cccctggggc	1920
52	tgtccaggac	tgggagttgc	agctttgtgt	taagctgac	acagacaccg	gctgcaccat	1980
53	cagcgggaag	cagagcccat	gtccaggatg	cctcctgctg	ccctgtgtcc	atccctagtc	2040
54	tgtcaggact	tcctgtcact	gttttccaaa	gctgtaaacc	tactgtgtga	acgttcacct	2100
55	taatgattga	ttctttaatc	tctgttttca	ctctcaggct	ctggtaagta	tttgtattct	2160
56	cttcatccca	gtctgattgc	atagccacac	tgcccggcac	gccacatcca	cccctgtctg	2220
57	cacatgagtt	gttctgacaa	cagcgtgtga	tacgtttcag	tttttccaca	ttgtccacgg	2280
58	ccagcacatg	aaagcatcac	ttctttttta	tgttgtggga	atctttgcaa	gttagtggtg	2340
59	catctgattt	tcaggtgtac	atttattttt	gactggggcag	ataggggatt	tttttttttt	2400
60	tccatgtccg	attcacacgc	tacacaccca	catgaacaca	ttcgaacttc	gaaggcacac	2460
61	actcctgctt	cataggcccc	acggtaagtg	agttcacacc	tagaacactg	tcctgaccgc	2520
62	aggacgcgtg	ccttggaactt	ggtattctac	atgtgactgg	ctttcttgcc	ctcgtctctt	2580
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72	actgacaaca	gtgggggtgag	gcttggccgt	ctgcttgacc	tggccccagg	tctataatth	180
73	tatgtaggat	ttccagccaa	aggtttccaa	gctttcagtt	ttgggacagg	tatggatgat	240
74	aaagggcacc	tgagcaatga	ggaagcacc	aaggctatca	aaccaccag	taaggagttc	300
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79	gatgtggaga	cagcttccga	ggggagcgtt	gaaagcagtt	ctgagatcag	aagtggccct	600
80	gtatctgact	ccttagggaa	agaacatcct	gcctcttctg	aaaaggcaaa	aggagggtgaa	660
81	gaggaagaag	acacctctga	cagtgcagct	gatggcctta	cgttgaagga	acttcagaac	720
82	cgccttcgga	gaaagcgaga	gcaagaacct	gtggagaggt	ccctgagagg	cagtcagaat	780
83	cgcctgagga	agaagcgag	agaggaagat	tctgccgaaa	ctgggagtg	ccaaataggc	840
84	agtgcggagc	aggacagacc	tctctgtaag	caggagcctg	aggctagtca	gggaccagtg	900
85	tcccagtcag	agacagatga	catagaaaat	cagttggaag	ggaaggcgac	tcagggaaat	960
86	acagaggaaa	acccagggga	agcgggcaaa	ccaaagcctg	agtgtgaggt	ttacgacccc	1020
87	aatgccctgt	actgcatctg	ccgccagcct	cacaacaaca	ggtttatgat	ctgctgtgat	1080
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91	ggcacagact	gcacaagcat	agggacagta	gagcagaagt	ccggagaaga	ccagggcata	1320
92	aagggtagga	ttgagaaggc	agcaaacccc	agcggcaaga	aaaaactcaa	gatattccag	1380
93	cctgtcgtag	aggctcctgg	tgtcctctaa	tgcattggcc	ctgggtgttc	cagtgtagca	1440
94	cagcctgact	ctgtgtattg	cagtaatgac	tgcattctca	aacacgcagc	agctaccatg	1500
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101     ctgggtggct gcctggggct gtctaggacc agagtcctgg gtgttctggt gctgatagta 1920
102     gccagcagct cactgccagc cagaagcaga taccaagatg cctctggacc ccagggtgtc 1980
103     ctgcctagcc tgtggagcct ctctgggtgg ttccataaaga gctgtgtagg cctcatgttg 2040
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107     ctcttctata gaaaagtgtat ttttttcatg agtttagggca tttttgaaag gacaggtaga 2280
108     caatttgtgt ctatttcaca tactacacac ctacataaac aggtttgaaat tttgaaggtc 2340
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116     ggggtgtgaac tcagagtgtt ggaccagcag tctaccagct gagctgcagt tctagccatg 2820
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127     20          25          30
128     Thr Ile Ala Lys Arg Glu Gly Ala Gly Asp Ala Glu Ala Asp Pro Leu
129     35          40          45
130     Glu Pro Pro Pro Pro Gln Gln Gln Leu Gly Leu Ser Leu Arg Arg Ser
131     50          55          60
132     Gly Arg Gln Pro Lys Arg Thr Glu Arg Val Glu Gln Phe Leu Thr Ile
133     65          70          75          80
134     Ala Arg Arg Arg Gly Arg Arg Ser Met Pro Val Ser Leu Glu Asp Ser
135     85          90          95
136     Gly Glu Pro Thr Ser Cys Pro Ala Thr Asp Ala Glu Thr Ala Ser Glu
137     100         105         110
138     Gly Ser Val Glu Ser Ala Ser Glu Thr Arg Ser Gly Pro Gln Ser Ala
139     115         120         125
140     Ser Thr Ala Val Lys Glu Arg Pro Ala Ser Ser Glu Lys Val Lys Gly
141     130         135         140
142     Gly Asp Asp His Asp Asp Thr Ser Asp Ser Asp Ser Asp Gly Leu Thr
143     145         150         155         160
144     Leu Lys Glu Leu Gln Asn Arg Leu Arg Arg Lys Arg Glu Gln Glu Pro
145     165         170         175
146     Thr Glu Arg Pro Leu Lys Gly Ile Gln Ser Arg Leu Arg Lys Lys Arg
147     180         185         190
148     Arg Glu Glu Gly Pro Ala Glu Thr Val Gly Ser Glu Ala Ser Asp Thr

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149          195          200          205
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152 Val Val Ser Gln Ala Gly Lys Asp Asp Arg Glu Ser Lys Leu Glu Gly
153          225          230          235          240
154 Lys Ala Ala Gln Asp Ile Lys Asp Glu Glu Pro Gly Asp Leu Gly Arg
155          245          250          255
156 Pro Lys Pro Glu Cys Glu Gly Tyr Asp Pro Asn Ala Leu Tyr Cys Ile
157          260          265          270
158 Cys Arg Gln Pro His Asn Asn Arg Phe Met Ile Cys Cys Asp Arg Cys
159          275          280          285
160 Glu Glu Trp Phe His Gly Asp Cys Val Gly Ile Ser Glu Ala Arg Gly
161          290          295          300
162 Arg Leu Leu Glu Arg Asn Gly Glu Asp Tyr Ile Cys Pro Asn Cys Thr
163          305          310          315          320
164 Ile Leu Gln Val Gln Asp Glu Thr His Ser Glu Thr Ala Asp Gln Gln
165          325          330          335
166 Glu Ala Lys Trp Arg Pro Gly Asp Ala Asp Gly Thr Asp Cys Thr Ser
167          340          345          350
168 Ile Gly Thr Ile Glu Gln Lys Ser Ser Glu Asp Gln Gly Ile Lys Gly
169          355          360          365
170 Arg Ile Glu Lys Ala Ala Asn Pro Ser Gly Lys Lys Lys Leu Lys Ile
171          370          375          380
172 Phe Gln Pro Val Ile Glu Ala Pro Gly Ala Ser Lys Cys Ile Gly Pro
173          385          390          395          400
174 Gly Cys Cys His Val Ala Gln Pro Asp Ser Val Tyr Cys Ser Asn Asp
175          405          410          415
176 Cys Ile Leu Lys His Ala Ala Ala Thr Met Lys Phe Leu Ser Ser Gly
177          420          425          430
178 Lys Glu Gln Lys Pro Lys Pro Lys Glu Lys Met Lys Met Lys Pro Glu
179          435          440          445
180 Lys Pro Ser Leu Pro Lys Cys Gly Ala Gln Ala Gly Ile Lys Ile Ser
181          450          455          460
182 Ser Val His Lys Arg Pro Ala Pro Glu Lys Lys Glu Thr Thr Val Lys
183          465          470          475          480
184 Lys Ala Val Val Val Pro Ala Arg Ser Glu Ala Leu Gly Lys Glu Ala
185          485          490          495
186 Ala Cys Glu Ser Ser Thr Pro Ser Trp Ala Ser Asp His Asn Tyr Asn
187          500          505          510
188 Ala Val Lys Pro Glu Lys Thr Ala Ala Pro Ser Pro Ser Leu Leu Tyr
189          515          520          525
190 Lys Cys Met Tyr His Leu Gly Val Gly Leu Leu Asp Pro Ser Arg Ser
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193          545          550          555          560
194 Leu Cys
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197 <211> LENGTH: 614
198 <212> TYPE: PRT

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206 35 40 45
207 Glu Gln Gln Pro Gln Gln His Asn Leu Ser Leu Arg Arg Ser Gly Arg
208 50 55 60
209 Gln Pro Lys Arg Thr Glu Arg Val Glu Glu Phe Leu Thr Thr Val Arg
210 65 70 75 80
211 Arg Arg Gly Lys Lys Asn Val Pro Val Ser Leu Glu Asp Ser Ser Glu
212 85 90 95
213 Pro Thr Ser Ser Thr Val Thr Asp Val Glu Thr Ala Ser Glu Gly Ser
214 100 105 110
215 Val Glu Ser Ser Ser Glu Ile Arg Ser Gly Pro Val Ser Asp Ser Leu
216 115 120 125
217 Gly Lys Glu His Pro Ala Ser Ser Glu Lys Ala Lys Gly Gly Glu Glu
218 130 135 140
219 Glu Glu Asp Thr Ser Asp Ser Asp Ser Asp Gly Leu Thr Leu Lys Glu
220 145 150 155 160
221 Leu Gln Asn Arg Leu Arg Arg Lys Arg Glu Gln Glu Pro Val Glu Arg
222 165 170 175
223 Ser Leu Arg Gly Ser Gln Asn Arg Leu Arg Lys Lys Arg Arg Glu Glu
224 180 185 190
225 Asp Ser Ala Glu Thr Gly Ser Val Gln Ile Gly Ser Ala Glu Gln Asp
226 195 200 205
227 Arg Pro Leu Cys Lys Gln Glu Pro Glu Ala Ser Gln Gly Pro Val Ser
228 210 215 220
229 Gln Ser Glu Thr Asp Asp Ile Glu Asn Gln Leu Glu Gly Lys Ala Thr
230 225 230 235 240
231 Gln Gly Asn Thr Glu Glu Asn Pro Arg Glu Ala Gly Lys Pro Lys Pro
232 245 250 255
233 Glu Cys Glu Val Tyr Asp Pro Asn Ala Leu Tyr Cys Ile Cys Arg Gln
234 260 265 270
235 Pro His Asn Asn Arg Phe Met Ile Cys Cys Asp Arg Cys Glu Glu Trp
236 275 280 285
237 Phe His Gly Asp Cys Val Gly Ile Ser Glu Ala Arg Gly Arg Leu Leu
238 290 295 300
239 Glu Arg Asn Gly Glu Asp Tyr Ile Cys Pro Asn Cys Thr Ile Leu Gln
240 305 310 315 320
241 Val Gln Asp Glu Thr Asn Gly Ser Ala Thr Asn Glu Gln Asp Ser Gly
242 325 330 335
243 Cys Arg Ser Val Gly Ala Asp Gly Thr Asp Cys Thr Ser Ile Gly Thr
244 340 345 350
245 Val Glu Gln Lys Ser Gly Glu Asp Gln Gly Ile Lys Gly Arg Ile Glu
246 355 360 365
247 Lys Ala Ala Asn Pro Ser Gly Lys Lys Lys Leu Lys Ile Phe Gln Pro

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